

Amendments to the Claims

This Listing of Claims will replace all prior versions and listings of claims in this application.

Listing of Claims

Claims 1-44 (Canceled).

Claim 45 (Previously amended). A culture-independent method of determining the abundance of an environmental parameter of interest by determining the abundance of at least one nucleic acid marker sequence, wherein the abundance of the nucleic acid marker sequence(s) correlates to the abundance of the environmental parameter, comprising the steps of:

- a. providing an environmental sample containing a population of interest;
- b. isolating genomic DNA from the environmental sample;
- c. assaying the genomic DNA by utilizing at least one pair of species-specific probes derived from genomic DNA that is specific to at least one of the nucleic acid marker sequences as PCR primers to determine the abundance of at least one of the nucleic acid marker sequences in the genomic DNA isolated from the sample; and
- d. inferring the abundance of the parameter of interest based upon the abundance of at least one of the nucleic acid marker sequences in the genomic DNA isolated from the sample.

Claim 46 (Previously presented). A culture-independent method of determining the abundance of an environmental parameter of interest by determining the abundance of at least one nucleic acid marker sequence, wherein the abundance of the nucleic acid marker sequence(s) correlates to the abundance of the environmental parameter, comprising the steps of:

- a. providing an environmental sample containing a population of interest;
- b. isolating genomic DNA from the environmental sample;

- c. assaying the genomic DNA by utilizing at least one ~~species-specific probe~~ derived from genomic DNA that is specific to at least one of the nucleic acid marker sequences as a hybridization probe to determine the abundance of at least one of the nucleic acid marker sequences in the genomic DNA isolated from the sample; and
- d. inferring the abundance of the parameter of interest based upon the abundance of at least one of the nucleic acid marker sequences in the genomic DNA isolated from the sample.

Claim 47 (Currently amended). The method according to claim 45 or claim 46, wherein the abundance of at least one of the nucleic acid markers shows a perfect correlation to the abundance of the parameter of interest, wherein the perfect correlation is expressed by an r-value of 1.

Claim 48 (Currently amended). The method according to claim 45 or claim 46, wherein the abundance of at least one of the nucleic acid markers shows a high degree of correlation to the abundance of the parameter of interest, wherein the high degree of correlation is expressed by an r-value of 0.8 to 0.99.

Claim 49 (Currently amended). The method according to claim 45 or claim 46, wherein the abundance of at least one of the nucleic acid markers shows a moderate degree of correlation to the abundance of the parameter of interest, wherein the moderate degree of correlation is expressed by an r-value of 0.5 to 0.7.

Claim 50 (Previously presented). The method according to claim 45 or claim 46, wherein the environmental parameter of interest is a subsurface oil or natural gas deposit.

Claim 51-56 (Canceled)

Claim 57 (Currently amended). The method of claim[[s]] 45 [[and]]or 46,
wherein the nucleic acid marker sequences are selected by a method comprising the steps of:

- a. providing a plurality of nucleic acid sequences whose abundance correlates to the abundance of the environmental parameter;
- b. ranking the nucleic acid sequences according to their level of correlation of their abundance to the abundance of the environmental parameter of interest;
- c. selecting at least one of the nucleic acid marker sequences from the set of nucleic acid sequences whose abundance has a high or moderate degree of correlation to the abundance of the environmental parameter.